Abstract

The present invention relates to methods and systems for sorting a plurality of protein structures generated by a database search based upon their corresponding sequences. The methods and systems according to the invention are based upon computer generated graphical user interfaces that present to the user: i) a multiple sequence alignment of the sequences corresponding to the structures to be sorted; ii) the means to identify whether one or more of the sequences comprise homologous alignment domains; and iii) the means to select one or more sequences for subsequent processing of their corresponding structures. In another aspect of the invention, the user is presented one or more phylogenetic tree representations of user selected homologous alignment domains so that the user may quickly determine the evolutionary similarity of a family of homologous alignment domains.